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SEQUENCE LISTING

<110> Kovesdi, Imre
Kessler, Paul

<120> VEGF FUSION PROTEINS

<130> 205654

<140> US 09/832,355

<141> 2001-04-10

<160> 126

<170> PatentIn version 3.0

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Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu
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35 40 45

Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
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Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile
65 70 75 80

Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe
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Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu
 50 55 60

Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly
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Arg Pro Lys Lys Asp
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Ala Arg Gln Glu Lys Cys
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Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
245 250 255

Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
260 265 270

Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
275 280 285

Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
290 295 300

Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
305 310 315 320

Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
325 330 335

Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
340 345 350

Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
355 360 365

Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
370 375 380

Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
385 390 395 400

Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
405 410 415

Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
420 425 430

Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
435 440 445

Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
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Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
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Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu
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Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln
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Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr
65 70 75 80

Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg
85 90 95

Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu
100 105 110

Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn
115 120 125

Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp
130 135 140

Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln
145 150 155 160

Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro
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Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe
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<213> Homo sapiens

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20 25 30

Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp Leu
35 40 45

Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met Ala
50 55 60

Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu Glu
65 70 75 80

Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys Leu
85 90 95

Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu Ile
100 105 110

Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln Leu
115 120 125

Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser Leu
130 135 140

Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu Leu

145 150 155 160
 Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr Arg
 165 170 175
 Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala Thr
 180 185 190
 Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp Thr
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 Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu Lys
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 Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg
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Glu

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 20 25 30
 Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg
 35 40 45
 Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys
 50 55 60
 Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys
 65 70 75 80
 Val His Ser Ile Met Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu
 85 90 95

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Ile	Ile	Gln	Arg	Arg	Glu	Asp	Gly	Ser	Val	Asp	Phe	Gln	Arg	Thr	Trp
	50					55					60				
Lys	Glu	Tyr	Lys	Val	Gly	Phe	Gly	Asn	Pro	Ser	Gly	Glu	Tyr	Trp	Leu
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Gly	Asn	Glu	Phe	Val	Ser	Gln	Leu	Thr	Asn	Gln	Gln	Arg	Tyr	Val	Leu
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Lys	Ile	His	Leu	Lys	Asp	Trp	Glu	Gly	Asn	Glu	Ala	Tyr	Ser	Leu	Tyr
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145					150					155					160
Lys	Cys	Ser	Gln	Met	Leu	Thr	Gly	Gly	Trp	Trp	Phe	Asp	Ala	Cys	Gly
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Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn Thr Asn
 180 185 190

Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser Gly Tyr Ser
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Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe
 210 215 220

<210> 22

<211> 219

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<213> Homo sapiens

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Lys Met Gly Pro Lys Gly Glu Pro Gly Pro Arg Asn Cys Arg Glu Leu
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 20 25 30

Glu Gly Arg Ala Leu Pro Val Phe Cys Asp Met Asp Thr Glu Gly Gly
 35 40 45

Gly Trp Leu Val Phe Gln Arg Arg Gln Asp Gly Ser Val Asp Phe Phe
 50 55 60

Arg Ser Trp Ser Ser Tyr Arg Ala Gly Phe Gly Asn Gln Glu Ser Glu
 65 70 75 80

Phe Trp Leu Gly Asn Glu Asn Leu His Gln Leu Thr Leu Gln Gly Asn
 85 90 95

Trp Glu Leu Arg Val Glu Leu Glu Asp Phe Asn Gly Asn Arg Thr Phe
 100 105 110

Ala His Tyr Ala Thr Phe Arg Leu Leu Gly Glu Val Asp His Tyr Gln
 115 120 125

Leu Ala Leu Gly Lys Phe Ser Glu Gly Thr Ala Gly Asp Ser Leu Ser
 130 135 140

Leu His Ser Gly Arg Pro Phe Thr Thr Tyr Asp Ala Asp His Asp Ser
 145 150 155 160

Ser Asn Ser Asn Cys Ala Val Ile Val His Gly Ala Trp Trp Tyr Ala
 165 170 175

Ser Cys Tyr Arg Ser Asn Leu Asn Gly Arg Tyr Ala Val Ser Glu Ala
 180 185 190

Ala Ala His Lys Tyr Gly Ile Asp Trp Ala Ser Gly Arg Gly Val Gly
 195 200 205

His Pro Tyr Arg Arg Val Arg Met Met Leu Arg
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<210> 23

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 <213> Homo sapiens

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Asp Cys Ser Ser Leu Tyr Gln Lys Asn Tyr Arg Ile Ser Gly Val Tyr
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Cys Asp Met Glu Thr Ser Gly Gly Gly Trp Thr Ile Ile Gln Arg Arg
          35          40          45

Lys Ser Gly Leu Val Ser Phe Tyr Arg Asp Trp Lys Gln Tyr Lys Gln
          50          55          60

Gly Phe Gly Ser Ile Arg Gly Asp Phe Trp Leu Gly Asn Glu His Ile
65          70          75          80

His Arg Leu Ser Arg Gln Pro Thr Arg Leu Arg Val Glu Met Glu Asp
          85          90          95

Trp Glu Gly Asn Leu Arg Tyr Ala Glu Tyr Ser His Phe Val Leu Gly
          100          105          110

Asn Glu Leu Asn Ser Tyr Arg Leu Phe Leu Gly Asn Tyr Thr Gly Asn
          115          120          125

Val Gly Asn Asp Ala Leu Gln Tyr His Asn Asn Thr Ala Phe Ser Thr
          130          135          140

Lys Asp Lys Asp Asn Asp Asn Cys Leu Asp Lys Cys Ala Gln Leu Arg
145          150          155          160

Lys Gly Gly Tyr Trp Tyr Asn Cys Cys Thr Asp Ser Asn Leu Asn Gly
          165          170          175

Val Tyr Tyr Arg Leu Gly Glu His Asn Lys His Leu Asp Gly Ile Thr
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Trp Tyr Gly Trp His Gly Ser Thr Tyr Ser Leu Lys Arg Val Glu Met
          195          200          205

Lys Ile Arg Pro Glu Asp Phe Lys Pro
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 <213> Homo sapiens

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Leu	Tyr	Gln	Arg	Gly	Gly	Trp	Trp	Tyr	His	Ala	Cys	Ala	His	Ser	Asn
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<213> Homo sapiens

<400> 25

Leu	Pro	Arg	Asp	Cys	Gln	Glu	Leu	Phe	Gln	Val	Gly	Glu	Arg	Gln	Ser
1				5					10					15	
Gly	Leu	Phe	Glu	Ile	Gln	Pro	Gln	Gly	Ser	Pro	Pro	Phe	Leu	Val	Asn
			20					25					30		
Cys	Lys	Met	Thr	Ser	Asp	Gly	Gly	Trp	Thr	Val	Ile	Gln	Arg	Arg	His
		35					40					45			
Asp	Gly	Ser	Val	Asp	Phe	Asn	Arg	Pro	Trp	Glu	Ala	Tyr	Lys	Ala	Gly
	50					55					60				
Phe	Gly	Asp	Pro	His	Gly	Glu	Phe	Trp	Leu	Gly	Leu	Glu	Lys	Val	His
	65					70					75				80

Ser Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp
 85 90 95
 Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly
 100 105 110
 Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln
 115 120 125
 Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser
 130 135 140
 Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys
 145 150 155 160
 Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu
 165 170 175
 Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys
 180 185 190
 Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln
 195 200 205
 Ala Thr Thr Met Leu Ile Gln
 210 215

<210> 26
 <211> 222
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Source not known

<400> 26

Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly
 1 5 10 15
 Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys
 20 25 30
 Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp
 35 40 45
 Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe
 50 55 60
 Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser
 65 70 75 80
 Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp
 85 90 95
 Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu

100	105	110
Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu		
115	120	125
Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr		
130	135	140
Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser		
145	150	155
Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn		
165	170	175
Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys Lys		
180	185	190
Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala		
195	200	205
Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala Ser		
210	215	220

<210> 27
 <211> 222
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Source not known

<400> 27

His Asp Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu	
1 5 10 15	
His Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe	
20 25 30	
His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln	
35 40 45	
His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr	
50 55 60	
Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu	
65 70 75 80	
Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu	
85 90 95	
Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr	
100 105 110	
Leu Gly Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr	
115 120 125	

Gly Asn Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser
 130 135 140

Thr Trp Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr
 145 150 155 160

Ser Gly Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn
 165 170 175

Gly Lys Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg
 180 185 190

Gly Leu Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser
 195 200 205

Thr Lys Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 210 215 220

<210> 28

<211> 214

<212> PRT

<213> Mus musculus

<400> 28

Arg Asp Cys Gln Glu Leu Phe Gln Glu Gly Glu Arg His Ser Gly Leu
 1 5 10 15

Phe Gln Ile Gln Pro Leu Gly Ser Pro Pro Phe Leu Val Asn Cys Glu
 20 25 30

Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg Leu Asn Gly
 35 40 45

Ser Val Asp Phe Asn Gln Ser Trp Glu Ala Tyr Lys Asp Gly Phe Gly
 50 55 60

Asp Pro Gln Gly Glu Phe Trp Leu Gly Leu Glu Lys Met His Ser Ile
 65 70 75 80

Thr Gly Asn Arg Gly Ser Gln Leu Ala Val Gln Leu Gln Asp Trp Asp
 85 90 95

Gly Asn Ala Lys Leu Leu Gln Phe Pro Ile His Leu Gly Gly Glu Asp
 100 105 110

Thr Ala Tyr Ser Leu Gln Leu Thr Glu Pro Thr Ala Asn Glu Leu Gly
 115 120 125

Ala Thr Asn Val Ser Pro Asn Gly Leu Ser Leu Pro Phe Ser Thr Trp
 130 135 140

Asp Gln Asp His Asp Leu Arg Gly Asp Leu Asn Cys Ala Lys Ser Leu
 145 150 155 160

Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly
 165 170 175

Gln Tyr Phe His Ser Ile Pro Arg Gln Arg Gln Glu Arg Lys Lys Gly

180 185 190
 Ile Phe Trp Lys Thr Trp Lys Gly Arg Tyr Tyr Pro Leu Gln Ala Thr
 195 200 205
 Thr Leu Leu Ile Gln Pro
 210
 <210> 29
 <211> 216
 <212> PRT
 <213> Homo sapiens
 <400> 29
 Phe Gln Asp Cys Ala Glu Ile Lys Arg Ser Gly Val Asn Thr Ser Gly
 1 5 10 15
 Val Tyr Thr Ile Tyr Glu Thr Asn Met Thr Lys Pro Leu Lys Val Phe
 20 25 30
 Cys Asp Met Glu Thr Asp Gly Gly Gly Trp Thr Leu Ile Gln His Arg
 35 40 45
 Glu Asp Gly Ser Val Asn Phe Gln Arg Thr Trp Glu Glu Tyr Lys Glu
 50 55 60
 Gly Phe Gly Asn Val Ala Arg Glu His Trp Leu Gly Asn Glu Ala Val
 65 70 75 80
 His Arg Leu Thr Ser Arg Thr Ala Tyr Leu Leu Arg Val Glu Leu His
 85 90 95
 Asp Trp Glu Gly Arg Gln Thr Ser Ile Gln Tyr Glu Asn Phe Gln Leu
 100 105 110
 Gly Ser Glu Arg Gln Arg Tyr Ser Leu Ser Val Asn Asp Ser Ser Ser
 115 120 125
 Ser Ala Gly Arg Lys Asn Ser Leu Ala Pro Gln Gly Thr Lys Phe Ser
 130 135 140
 Thr Lys Asp Met Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Gln Met
 145 150 155 160
 Leu Ser Gly Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn
 165 170 175
 Gly Ile Tyr Tyr Ser Val His Gln His Leu His Lys Ile Asn Gly Ile
 180 185 190
 Arg Trp His Tyr Phe Arg Gly Pro Ser Tyr Ser Leu His Gly Thr Arg
 195 200 205
 Met Met Leu Arg Pro Met Gly Ala
 210 215
 <210> 30
 <211> 216

<212> PRT

<213> Homo sapiens

<400> 30

Phe Gln Asp Cys Ala Glu Ile Gln Arg Ser Gly Ala Ser Ala Ser Gly
 1 5 10 15

Val Tyr Thr Ile Gln Val Ser Asn Ala Thr Lys Pro Arg Lys Val Phe
 20 25 30

Cys Asp Leu Gln Ser Ser Gly Gly Arg Trp Thr Leu Ile Gln Arg Arg
 35 40 45

Glu Asn Gly Thr Val Asn Phe Gln Arg Asn Trp Lys Asp Tyr Lys Gln
 50 55 60

Gly Phe Gly Asp Pro Ala Gly Glu His Trp Leu Gly Asn Glu Val Val
 65 70 75 80

His Gln Leu Thr Arg Arg Ala Ala Tyr Ser Leu Arg Val Glu Leu Gln
 85 90 95

Asp Trp Glu Gly His Glu Ala Tyr Ala Gln Tyr Glu His Phe His Leu
 100 105 110

Gly Ser Glu Asn Gln Leu Tyr Arg Leu Ser Val Val Gly Tyr Ser Gly
 115 120 125

Ser Ala Gly Arg Gln Ser Ser Leu Val Leu Gln Asn Thr Ser Phe Ser
 130 135 140

Thr Leu Asp Ser Asp Asn Asp His Cys Leu Cys Lys Cys Ala Gln Val
 145 150 155 160

Met Ser Gly Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn
 165 170 175

Gly Val Tyr Tyr His Ala Pro Asp Asn Lys Tyr Lys Met Asp Gly Ile
 180 185 190

Arg Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ala Ser Arg
 195 200 205

Met Met Ile Arg Pro Leu Asp Ile
 210 215

<210> 31

<211> 224

<212> PRT

<213> Homo sapiens

<400> 31

Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
 1 5 10 15

His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg
 20 25 30

<400> 32

Ile	Asn	Glu	Gly	Pro	Phe	Lys	Asp	Cys	Gln	Gln	Ala	Lys	Glu	Ala	Gly
1				5					10					15	
His	Ser	Val	Ser	Gly	Ile	Tyr	Met	Ile	Lys	Pro	Glu	Asn	Ser	Asn	Gly
			20					25					30		
Pro	Met	Gln	Leu	Trp	Cys	Glu	Asn	Ser	Leu	Asp	Pro	Gly	Gly	Trp	Thr
		35					40					45			
Val	Ile	Gln	Lys	Arg	Thr	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Asn	Trp
	50					55					60				
Glu	Asn	Tyr	Lys	Lys	Gly	Phe	Gly	Asn	Ile	Asp	Gly	Glu	Tyr	Trp	Leu
65					70					75					80

22

<400> 33

Gly 1	Lys	Lys	Glu 5	Lys	Pro	Glu	Lys	Lys	Val 10	Lys	Lys	Ser	Asp	Cys 15	Gly
Glu	Trp	Gln	Trp 20	Ser	Val	Cys	Val	Pro 25	Thr	Ser	Gly	Asp	Cys 30	Gly	Leu
Gly	Thr	Arg 35	Glu	Gly	Thr	Arg	Thr 40	Gly	Ala	Glu	Cys	Lys 45	Gln	Thr	Met
Lys	Thr 50	Gln	Arg	Cys	Lys	Ile 55	Pro	Cys	Asn	Trp	Lys 60	Lys	Gln	Phe	Gly
Ala 65	Glu	Cys	Lys	Tyr	Gln 70	Phe	Gln	Ala	Trp	Gly 75	Glu	Cys	Asp	Leu	Asn 80
Thr	Ala	Leu	Lys 85	Thr	Arg	Thr	Gly	Ser 90	Leu	Lys	Arg	Ala	Leu	His 95	Asn
Ala	Glu	Cys	Gln 100	Lys	Thr	Val	Thr	Ile 105	Ser	Lys	Pro	Cys	Gly 110	Lys	Leu
Thr	Lys 115	Pro	Lys	Pro	Gln	Ala	Glu 120	Ser	Lys	Lys	Lys	Lys 125	Lys	Glu	Gly
Lys	Lys	Gln	Glu	Lys	Met	Leu	Asp								

130

135

<210> 34
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 34

Lys Lys Lys Asp Lys Val Lys Lys Gly Gly Pro Gly Ser Glu Cys Ala
 1 5 10 15
 Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser Ser Lys Asp Cys Gly Val
 20 25 30
 Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln Thr Gln Arg Ile Arg Cys
 35 40 45
 Arg Val Pro Cys Asn Trp Lys Lys Glu Phe Gly Ala Asp Cys Lys Tyr
 50 55 60
 Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr Lys Val
 65 70 75 80
 Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys Gln Glu
 85 90 95
 Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr Lys Ala Lys Ala
 100 105 110
 Lys Ala Lys Lys Gly Lys Gly Lys Asp
 115 120

<210> 35
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 35

Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn Thr Ala
 1 5 10 15
 Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn Ala Glu
 20 25 30
 Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys
 35 40

<210> 36
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 36

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
 1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
 35 40 45

Thr Lys Pro Lys Pro Gln
 50

<210> 37

<211> 72

<212> PRT

<213> Homo sapiens

<400> 37

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
 1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
 35 40 45

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Lys Glu Gly
 50 55 60

Lys Lys Gln Glu Lys Met Leu Asp
 65 70

<210> 38

<211> 80

<212> PRT

<213> Homo sapiens

<400> 38

Cys Gly Glu Trp Thr Trp Gly Pro Cys Ile Pro Asn Ser Lys Asp Cys
 1 5 10 15

Gly Leu Gly Thr Arg Glu Gly Thr Cys Lys Gln Glu Thr Arg Lys Leu
 20 25 30

Lys Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly Ala Asp Cys
 35 40 45

Lys Tyr Lys Phe Glu Ser Trp Gly Glu Cys Asp Ala Asn Thr Gly Leu
 50 55 60

Lys Thr Arg Ser Gly Thr Leu Lys Lys Ala Leu Tyr Asn Ala Asp Cys
 65 70 75 80

<210> 39

<211> 21

<212> PRT

<213> Homo sapiens

<400> 39

Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
 1 5 10 15

Glu Trp Gln Trp Ser
 20

<210> 40
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 40

Ser Lys Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp
 1 5 10 15

<210> 41
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 41

Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr
 1 5 10 15

Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala
 20 25 30

Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr
 35 40 45

Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 50 55 60

<210> 42
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 42

Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr
 1 5 10 15

Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys
 20 25 30

Gln Glu Thr Ile Arg Val Thr Lys Pro Cys
 35 40

<210> 43
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 43

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
 1 5 10 15

Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
 20 25 30

<210> 44
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 44

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

Leu Thr Ser Ala
 20

<210> 45
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 45

Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys
 1 5 10 15

Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp
 20 25 30

Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala
 35 40 45

Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr
 50 55 60

Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn
 65 70 75 80

Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr
 85 90 95

Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys
 100 105 110

Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys
 115 120 125

Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser
 130 135

<210> 46
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys
 1 5 10 15

<210> 47
 <211> 8
 <212> PRT
 <213> Homo sapiens

<400> 47

Lys Lys Asn Gly Ser Cys Lys Arg
 1 5

<210> 48
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<220>
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 <222> (5)..(5)
 <223> "Xaa" may be between 5 and 7 of any amino acids

<220>
 <221> misc_feature
 <222> (7)..(9)
 <223> "Xaa" may be any amino acid

<400> 48

Arg Leu Tyr Cys Xaa Leu Xaa Xaa Xaa Pro Asp Gly Arg
 1 5 10

<210> 49
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 49

Ile Ser Ser Lys
 1

<210> 50
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 50

Lys Lys Pro Lys Leu
 1 5

<210> 51
 <211> 535
 <212> PRT
 <213> Homo sapiens

<400> 51

Met	Leu	Gly	Pro	Cys	Met	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Arg	1	5	10	15
Leu	Gln	Leu	Ser	Leu	Gly	Ile	Ile	Pro	Val	Glu	Glu	Glu	Asn	Pro	Asp	20	25	30
Phe	Trp	Asn	Arg	Glu	Ala	Ala	Glu	Ala	Leu	Gly	Ala	Ala	Lys	Lys	Leu	35	40	45
Gln	Pro	Ala	Gln	Thr	Ala	Ala	Lys	Asn	Leu	Ile	Ile	Phe	Leu	Gly	Asp	50	55	60
Gly	Met	Gly	Val	Ser	Thr	Val	Thr	Ala	Ala	Arg	Ile	Leu	Lys	Gly	Gln	65	70	75
Lys	Lys	Asp	Lys	Leu	Gly	Pro	Glu	Ile	Pro	Leu	Ala	Met	Asp	Arg	Phe	85	90	95
Pro	Tyr	Val	Ala	Leu	Ser	Lys	Thr	Tyr	Asn	Val	Asp	Lys	His	Val	Pro	100	105	110
Asp	Ser	Gly	Ala	Thr	Ala	Thr	Ala	Tyr	Leu	Cys	Gly	Val	Lys	Gly	Asn	115	120	125
Phe	Gln	Thr	Ile	Gly	Leu	Ser	Ala	Ala	Ala	Arg	Phe	Asn	Gln	Cys	Asn	130	135	140
Thr	Thr	Arg	Gly	Asn	Glu	Val	Ile	Ser	Val	Met	Asn	Arg	Ala	Lys	Lys	145	150	155
Ala	Gly	Lys	Ser	Val	Gly	Val	Val	Thr	Thr	Thr	Arg	Val	Gln	His	Ala	165	170	175
Ser	Pro	Ala	Gly	Thr	Tyr	Ala	His	Thr	Val	Asn	Arg	Asn	Trp	Tyr	Ser	180	185	190
Asp	Ala	Asp	Val	Pro	Ala	Ser	Ala	Arg	Gln	Glu	Gly	Cys	Gln	Asp	Ile	195	200	205
Ala	Thr	Gln	Leu	Ile	Ser	Asn	Met	Asp	Ile	Asp	Val	Ile	Leu	Gly	Gly	210	215	220
Gly	Arg	Lys	Tyr	Met	Phe	Arg	Met	Gly	Thr	Pro	Asp	Pro	Glu	Tyr	Pro	225	230	235
Asp	Asp	Tyr	Ser	Gln	Gly	Gly	Thr	Arg	Leu	Asp	Gly	Lys	Asn	Leu	Val	245	250	255
Gln	Glu	Trp	Leu	Ala	Lys	Arg	Gln	Gly	Ala	Arg	Tyr	Val	Trp	Asn	Arg	260	265	270
Thr	Glu	Leu	Met	Gln	Ala	Ser	Leu	Asp	Pro	Ser	Val	Thr	His	Leu	Met			

275	280	285
Gly Leu Phe Glu Pro Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser		
290	295	300
Thr Leu Asp Pro Ser Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu		
305	310	315
Leu Ser Arg Asn Pro Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg		
	325	330
Ile Asp His Gly His His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu		
	340	345
Thr Ile Met Phe Asp Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser		
	355	360
Glu Glu Asp Thr Leu Ser Leu Val Thr Ala Asp His Ser His Val Phe		
	370	375
Ser Phe Gly Gly Tyr Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala		
385	390	395
Pro Gly Lys Ala Arg Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly		
	405	410
Asn Gly Pro Gly Tyr Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr		
	420	425
Glu Ser Glu Ser Gly Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro		
	435	440
Leu Asp Glu Glu Thr His Ala Gly Glu Asp Val Ala Val Phe Ala Arg		
	450	455
Gly Pro Gln Ala His Leu Val His Gly Val Gln Glu Gln Thr Phe Ile		
465	470	475
Ala His Val Met Ala Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys		
	485	490
Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala His Pro Gly Arg		
	500	505
Ser Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu		
	515	520
Leu Glu Thr Ala Thr Ala Pro		
530	535	
<210> 52		
<211> 22		
<212> PRT		
<213> Homo sapiens		
<400> 52		
Met Leu Gly Pro Cys Met Leu Leu Leu Leu Leu Leu Leu Gly Leu Arg		
1	5	10
		15

Leu Gln Leu Ser Leu Gly
20

<210> 53
<211> 29
<212> PRT
<213> Homo sapiens

<400> 53

Ala Ala His Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu
1 5 10 15

Ala Gly Thr Leu Leu Leu Leu Glu Thr Ala Thr Ala Pro
20 25

<210> 54
<211> 108
<212> PRT
<213> Homo sapiens

<400> 54

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln
1 5 10 15

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe
20 25 30

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro
35 40 45

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn
50 55 60

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn
65 70 75 80

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys
85 90 95

Ala Gly Lys Ser Val Gly Val Val Thr Thr Thr Arg
100 105

<210> 55
<211> 20
<212> PRT
<213> Artificial sequence

<220>
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<222> ()..()
<223> Synthetic

<220>
<221> misc_feature
<222> (8)..(8)
<223> "Xaa" may be any amino acid

<400> 55

Ala	Gln	Val	Pro	Asp	Ser	Ala	Xaa	Thr	Ala	Thr	Ala	Tyr	Leu	Cys	Gly
1				5				10						15	

Val	Lys	Ala	Asn
			20

<210> 56

<211> 86

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<220>

<221> misc_feature

<222> (7)..(7)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (30)..(30)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (33)..(34)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (36)..(36)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (39)..(39)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (41)..(41)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (44)..(44)

<223> "Xaa" may be any amino acid

<220>

<221> misc_feature

<222> (47)..(47)

<223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (56)..(57)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (65)..(65)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (78)..(79)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (81)..(81)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (83)..(83)
 <223> "Xaa" may be any amino acid

<400> 56

Thr Asn Val Ala Lys Asn Xaa Ile Met Phe Leu Gly Asp Gly Met Gly
 1 5 10 15

Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Xaa His His
 20 25 30

Xaa Xaa Gly Xaa Glu Thr Xaa Leu Xaa Met Asp Xaa Phe Pro Xaa Val
 35 40 45

Ala Leu Ser Lys Thr Tyr Asn Xaa Xaa Ala Gln Val Pro Asp Ser Ala
 50 55 60

Xaa Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Ala Asn Xaa Xaa Thr
 65 70 75 80

Xaa Gly Xaa Ser Ala Ala
 85

<210> 57
 <211> 53
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (22)..(22)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (34)..(35)
 <223> "Xaa" may be any amino acid

<220>
 <221> misc_feature
 <222> (41)..(42)
 <223> "Xaa" may be any amino acid

<400> 57

Glu Asp Thr Leu Thr Xaa Val Thr Ala Asp His Ser His Val Phe Xaa
 1 5 10 15

Phe Gly Gly Tyr Thr Xaa Arg Gly Asn Ser Ile Phe Gly Leu Ala Pro
 20 25 30

Met Xaa Xaa Asp Thr Asp Lys Lys Xaa Xaa Thr Ala Ile Leu Tyr Gly
 35 40 45

Asn Gly Pro Gly Tyr
 50

<210> 58
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 58

Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu Leu
 1 5 10 15

Glu Thr Ala Thr Ala Pro
 20

<210> 59
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 59

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly

				20					25					30			
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln		
		35					40					45					
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu		
	50					55					60						
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu		
65					70				75						80		
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro		
				85					90					95			
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His		
			100					105					110				
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys		
		115					120					125					
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Lys	Ser	Val		
	130					135					140						
Arg	Gly	Lys	Gly	Cys	Asp	Lys	Pro	Arg	Arg								
145					150												
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<213>	Artificial sequence																
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<222>	()..()																
<223>	Synthetic																
<400>	60																
Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu		
1				5					10					15			
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly		
			20					25					30				
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln		
		35					40					45					
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu		
	50					55					60						
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu		
65					70				75						80		
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro		
				85					90					95			
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His		
			100					105					110				

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
 130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Cys Asp Lys Pro
 145 150 155 160

Arg Arg

<210> 61
 <211> 150
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 61

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys Lys
 130 135 140

Cys Asp Lys Pro Arg Arg
 145 150

<210> 62
 <211> 154
 <212> PRT
 <213> Artificial sequence

<220>

<221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 62

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys Lys
 130 135 140

Lys Lys Lys Lys Cys Asp Lys Pro Arg Arg
 145 150

<210> 63
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 63

Gly Gly Gly Gly Ser Ser Ser
 1 5

<210> 64
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()

<223> Synthetic

<400> 64

Ile Glu Gly Arg
1

<210> 65

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 65

Pro Gly Ile Ser Gly Gly Gly Gly Gly
1 5

<210> 66

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 66

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 67

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 67

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Lys Glu Phe
1 5 10

<210> 68

<211> 26

<212> PRT

<213> Homo sapiens

<400> 68

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Val Leu His His Ala Lys Trp Ser Gln Ala
 20 25

<210> 69
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 69
 cgcggaacca ccatgaactt tctgctgtct tgg 33

<210> 70
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 70
 ctaaattggtt tctcttcttc cccgcctcgg ctgtgcaca 39

<210> 71
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 71
 tgtgacaagc ctgaggcggg aggaagagaa accatttag 39

<210> 72
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 72
 cgcggaacct caaaaatcta aaggtcga 28

<210> 73

<211> 1107
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 73
 gctgcaccca tggcagaagg aggagggcag aatcatcacg aagtggtgaa gttcatggat 60
 gtctatcagc gcagctactg ccatccaatc gagaccctgg tggacatctt ccaggagtac 120
 cctgatgaga tcgagtacat cttcaagcca atgaactttc tgctgtcttg ggtgcattgg 180
 agccttgcc tgcgtgctcta cctccaccat gccaaagtggc cccagtcctg tgtgcccctg 240
 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420
 aaatgtgaca agccgaggcg ggaggaagag aaaccattta gagactgtgc agatgtatat 480
 caagctgggt ttaataaaaag tgaatctac actattttata ttaataatat gccagaaccc 540
 aaaaagggtg tttgcaatat ggatgtcaat gggggagggt ggactgtaat acaacatcgt 600
 gaagatggaa gtctagattt ccaaagaggc tgaaggaat ataaaatggg ttttggaat 660
 ccctccggtg aatattggct ggggaatgag tttatTTTTg ccattaccag tcagaggcag 720
 tacatgctaa gaattgagtt aatggactgg gaagggaacc gagcctattc acagtatgac 780
 agattccaca taggaaatga aaagcaaac tataggttgt atttaaaagg tcacactggg 840
 acagcaggaa aacagagcag cctgatctta cacggtgctg atttcagcac taaagatgct 900
 gataatgaca actgtatgtg caaatgtgcc ctcatgttaa caggaggatg gtggtttgat 960
 gcttgtggcc cctccaatct aaatggaatg ttctatactg cgggacaaaa ccatggaaaa 1020
 ctgaatggga taaagtggca ctacttcaaa gggcccagtt actccttacg ttccacaact 1080
 atgatgattc gacctttaga tttttga 1107

<210> 74
 <211> 368
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 74

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140
 Pro Arg Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr
 145 150 155 160
 Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn
 165 170 175
 Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly
 180 185 190
 Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln
 195 200 205
 Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu
 210 215 220
 Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln
 225 230 235 240
 Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr
 245 250 255
 Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg
 260 265 270
 Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu
 275 280 285
 Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn
 290 295 300
 Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp

<400> 78
 atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgctcta cctccaccat 60
 gccaaagtggc cccaggctgc acccatggca gaaggaggag gccagaatca tcacgaagtg 120
 gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180
 atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240
 atgcgatgcg ggggctgctg caatgacgag ggccctggagt gtgtgcccac tgaggagtcc 300
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420
 aaatgtgaca agccgaggcg gcaatttggc gcggagtgc aataccagtt ccaggcctgg 480
 ggagaatgtg acctgaacac agccctgaag accagaactg gaagtctgaa gcgagccctg 540
 cacaatgccg aatgccagaa gactgtcacc atctccaagc cctgtggcaa actgaccaag 600
 cccaaacctc aagcagaatc taagaagaag aaaaaggaag gcaagaaaca ggagaagatg 660
 ctggattaa 669

<210> 79
 <211> 222
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 79

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu
1			5						10					15	
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly
			20					25					30		
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln
		35					40					45			
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu
	50					55					60				
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu
65				70					75					80	
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro
			85					90						95	
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His
			100					105						110	

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140

Pro Arg Arg Gln Phe Gly Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp
 145 150 155 160

Gly Glu Cys Asp Leu Asn Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu
 165 170 175

Lys Arg Ala Leu His Asn Ala Glu Cys Gln Lys Thr Val Thr Ile Ser
 180 185 190

Lys Pro Cys Gly Lys Leu Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys
 195 200 205

Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp
 210 215 220

<210> 80
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 80
 tgcagtcggc tccaaactcc cgctcggt tgtcaca

37

<210> 81
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 81
 tgtgacaagc cgaggcggga gtttggagcc gactgca

37

<210> 82
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 82
 cgcgatccc tagtcctttc ccttccc

27

<210> 83
 <211> 639
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 83
 atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgtctta cctccaccat 60
 gccaaagtggc cccaggtgc acccatggca gaaggaggag ggcagaatca tcacgaagtg 120
 gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180
 atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgccctg 240
 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420
 aaatgtgaca agccgaggcg ggagtttggg gccgactgca agtacaagtt tgagaactgg 480
 ggtgcgtgtg atggggggcac aggcaccaa gtccgccaag gcaccctgaa gaaggcgcg 540
 tacaatgctc agtgccagga gaccatccgc gtcaccaagc cctgcacccc caagaccaa 600
 gcaaaggcca aagccaagaa agggaaggga aaggactag 639

<210> 84
 <211> 212
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 84

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu


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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 87
cgcgatcct tagtgaagg tggtgggg                                     28

<210> 88
<211> 1116
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 88
atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgtctta cctccaccat      60
gccaagtggg cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg      120
gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctgggtggac      180
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg      240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc      300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa      420
aaatgtgaca agccgaggcg gaagccgtcg ggcccatgga gagactgcct gcaggccctg      480
gaggatggcc acgacaccag ctccatctac ctgggtgaagc cggagaacac caaccgcctc      540
atgcaggtgt ggtgcgacca gagacacgac cccggggggct ggaccgtcat ccagagacgc      600
ctggatggct ctgttaactt cttcaggaac tgggagacgt acaagcaagg gtttggaac      660
attgatggcg aatactggct gggcctggag aacatttact ggctgacgaa ccaaggcaac      720
tacaaactcc tggtgaccat ggaggactgg tccggccgca aagtctttgc agaatacgcc      780
agtttccgcc tggaaacctga gagcgagtat tataagctgc ggctggggcg ctaccatggc      840
aatgcgggtg actcctttac atggcacaac ggcaagcagt tcaccaccct ggacagagat      900
catgatgtct acacaggaaa ctgtgcccac taccagaagg gaggctgggtg gtataacgcc      960
tgtgcccact ccaacctcaa cggggtctgg taccgcgggg gccattaccg gagccgctac     1020
caggacggag tctactgggc tgagttccga ggaggctctt actcactcaa gaaagtgggtg     1080
atgatgatcc gaccgaaccc caacaccttc cactaa                               1116

<210> 89

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<211> 371
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 89

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140

Pro Arg Arg Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu
 145 150 155 160

Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn
 165 170 175

Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly
 180 185 190

Gly Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
 195 200 205

Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu
 210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn
 225 230 235 240

Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe
 245 250 255

Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys
 260 265 270

Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp
 275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr
 290 295 300

Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala
 305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr
 325 330 335

Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly
 340 345 350

Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn
 355 360 365

Thr Phe His
 370

<210> 90
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 90
 gaatggtcct tcattgatcc gcctcggtt gtcaca

36

<210> 91
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 91
 tgtgacaagc cgaggcgat caatgaagga ccattc

36

<210> 92
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 92
cgcggtacct cagtcaatag gcttgatca 29

<210> 93
<211> 1104
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 93
atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgctcta cctccaccat 60
gccaagtggg cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg 120
gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctgggtggac 180
atcttcagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420
aaatgtgaca agccgaggcg gatcaatgaa ggaccattca aagactgtca gcaagcaaaa 480
gaagctgggc attcgggtcag tgggatttat atgattaaac ctgaaaacag caatggacca 540
atgcagttat ggtgtgaaaa cagtttggac cctggggggt ggactgttat tcagaaaaga 600
acagacggct ctgtcaactt cttcagaaat tgggaaaatt ataagaaagg gtttggaaac 660
attgacggag aatactggct tggactggaa aatatctata tgcttagcaa tcaagataat 720
tacaagttat tgattgaatt agaagactgg agtgataaaa aagtctatgc agaatacagc 780
agctttcgtc tggaaacctga aagtgaattc tatagactgc gcctgggaac ttaccagggg 840
aatgcagggg attctatgat gtggcataat ggtaaacaat tcaccacact ggacagagat 900
aaagatatgt atgcaggaaa ctgcgcccac tttcataaag gaggctgggtg gtacaatgcc 960
tgtgcacatt ctaacctaaa tggagtatgg tacagaggag gccattacag aagcaagcac 1020
caagatggaa ttttctgggc cgaatacaga ggcgggtcat actccttaag agcagttcag 1080
atgatgatca agcctattga ctga 1104

<210> 94
<211> 367
<212> PRT
<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 94

```

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1          5          10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
          20          25          30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
          35          40          45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50          55          60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65          70          75          80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
          85          90          95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
          100          105          110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
          115          120          125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
          130          135          140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys
145          150          155          160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
          165          170          175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly
          180          185          190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe
          195          200          205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu
210          215          220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn
225          230          235          240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr
          245          250          255

Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg
          260          265          270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp
275          280          285

```

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr
 290 295 300

Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala
 305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr
 325 330 335

Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly
 340 345 350

Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
 355 360 365

<210> 95
 <211> 1387
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (1201)..(1219)
 <223> "n" may be any nucleotide

<220>
 <221> misc_feature
 <222> (1295)..(1324)
 <223> "n" may be any nucleotide

<400> 95
 atgtggcaga ttgttttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60
 aactttcggg agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc 120
 tgcagctaca ctttcctcct gccagagatg gacaactgcc gctcttcctc cagcccctac 180
 gtgtccaatg ctgtgcagag ggacgcgccg ctccaatacg atgactcggg gcagaggctg 240
 caagtgcctg agaacatcat ggaaaacaac actcagtggc taatgaaggt agagaatata 300
 tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag 360
 acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420
 aagttaactg atgtggaagc ccaagtatta aatcagacca cgagacttga acttcagctc 480
 ttggaacact ccctctcgac aaacaaattg gaaaaacaga ttttggacca gaccagtga 540
 ataaacaaat tgcaagataa gaacagtttc ctagaaaaga aggtgctagc tatggaagac 600
 aagcacatca tccaactaca gtcaataaaa gaagagaaag atcagctaca ggtgttagta 660

```

tccaagcaga attccatcat tgaagaactc gaaaaaaaaa tagtgactgc cacgggtgaat 720
aattcagttc ttcagaagca gcaacatgat ctcatggaga cagttaataa cttactgact 780
atgatgtcca catcaaacgc agctaaggac cccactgttg ctaaagaaga acaaatcagc 840
ttcagagact gtgctgaagt attcaaatca ggacacacca cgaatggcat ctacacgtta 900
acattcccta attctacaga agagatcaag gcctactgtg acatggaagc tggaggaggc 960
gggtggacaa ttattcagcg acgtgaggat ggacagcgtt catttcagag gacttggaaa 1020
gaatataaag tgggatttgg taacctctca gaaaaatatt ggctgggaaa tgagtttgtt 1080
tcgcaactga ctaatcagca acgctatgtg cttaaaatac accttaaaga ctgggaaggg 1140
aatgaggctt actcattgta tgaacatttc tatctctcaa gtgaagaact caattatagg 1200
nnnnnnnnnn nnnnnnnnng gcaatgattt tagcacaagg gatggagcca ccgncanatg 1260
tatttgcaaa tggtcacaaa tgctaacagn aggtnnnnnn nnnnnnnnnn nnnnnnnnnn 1320
nnnntactgg aaaggctcag gctattcgct caaggccaca accatgatga tccgaccagc 1380
agatttc 1387

```

```

<210> 96
<211> 360
<212> PRT
<213> Artificial sequence

```

```

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

```

```

<220>
<221> misc_feature
<222> (269)..(272)
<223> "Xaa" may be any amino acid

```

```

<400> 96

```

```

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1             5             10             15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20             25             30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35             40             45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50             55             60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65             70             75             80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys

```

85										90					95				
Leu	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met	Val	Glu	Ile				
			100					105						110					
Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile	Glu	Ile	Gly				
		115					120					125							
Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys	Leu	Thr	Asp				
	130					135					140								
Val	Glu	Ala	Gln	Val	Ser	Asn	Ala	Thr	Thr	Arg	Leu	Glu	Leu	Gln	Leu				
	145				150						155				160				
Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln	Ile	Leu	Asp				
			165						170					175					
Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser	Phe	Leu	Glu				
		180					185						190						
Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln	Leu	Gln	Ser				
		195					200					205							
Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser	Lys	Gln	Asn				
	210					215					220								
Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala	Thr	Val	Asn				
	225				230						235				240				
Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	His	Asp	Leu	Met	Glu	Thr	Val	Asn				
			245						250					255					
Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Cys	Lys	Xaa	Xaa	Xaa	Xaa				
		260						265				270							
Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Phe	Arg	Asp	Cys	Ala	Glu	Val	Phe				
		275					280					285							
Lys	Ser	Gly	His	Thr	Thr	Asn	Gly	Ile	Tyr	Thr	Leu	Met	Trp	Gln	Ile				
	290					295					300								
Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala	Ala	Ala	Tyr	Asn				
	305				310						315				320				
Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys	Gln	Tyr	Gln	Val				
			325						330					335					
Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro	Glu	Met	Asp	Asn				
		340						345					350						
Cys	Arg	Ser	Ser	Ser	Ser	Pro	Tyr												
		355					360												

<210> 97

<211> 339

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 97

```

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1          5          10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
          20          25          30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
          35          40          45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50          55          60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65          70          75          80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
          85          90          95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
          100          105          110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115          120          125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130          135          140

Pro Arg Arg Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val
145          150          155          160

Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu
          165          170          175

Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro
          180          185          190

Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser
195          200          205

Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn
210          215          220

Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln
225          230          235          240

Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln
          245          250          255

Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp
          260          265          270

Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp
275          280          285

```

Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr
 290 295 300

Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe
 305 310 315 320

Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro
 325 330 335

Leu Asp Phe

<210> 98
 <211> 361
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 98
 gtccaatgct gtgcagaggg acgcgccgct cgaatacgat gactcgggtgc agaggctgca 60
 agtgctggag aacatcatgg aaaacaacac tcagtggcta atgaaggtag agaatatatc 120
 ccaggacaac atgaagaaaag aaatggtaga gatacagcag aatgcagtac agaaccagac 180
 ggctgtgatg atagaaatag ggacaaacct gttgaaccaa acagcggagc aaacgcggaa 240
 gttaactgat gtggaagccc aagtattaaa tcagaccacg agacttgaac ttcagctctt 300
 ggaacactcc ctctcgacaa acaaattgga aaaacagatt ttggaccaga ccagtgaaat 360
 a 361

<210> 99
 <211> 123
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 99

Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser
 1 5 10 15

Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln
 20 25 30

Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu
 35 40 45

Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met

50	55	60
Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg		
65	70	75 80
Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu		
	85	90 95
Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys		
	100	105 110
Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys		
	115	120

<210> 100
 <211> 462
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 100

Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser		
1	5	10 15
Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln		
	20	25 30
Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu		
	35	40 45
Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met		
	50	55 60
Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg		
65	70	75 80
Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu		
	85	90 95
Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys		
	100	105 110
Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Met Asn Phe Leu Leu		
	115	120 125
Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu Tyr Leu His His Ala		
	130	135 140
Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His		
145	150	155 160
His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His		
	165	170 175

Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile
 180 185 190
 Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly
 195 200 205
 Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn
 210 215 220
 Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile
 225 230 235 240
 Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys
 245 250 255
 Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg Arg Met Pro
 260 265 270
 Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp
 275 280 285
 Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly
 290 295 300
 Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp
 305 310 315 320
 Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met
 325 330 335
 Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln
 340 345 350
 Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr
 355 360 365
 Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu
 370 375 380
 His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met
 385 390 395 400
 Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys
 405 410 415
 Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His
 420 425 430
 Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr
 435 440 445
 Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe
 450 455 460
 <210> 101
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 101

Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
 1 5 10 15
 His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg
 20 25 30
 Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr
 35 40 45
 Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp
 50 55 60
 Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu
 65 70 75 80
 Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu
 85 90 95
 Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr
 100 105 110
 Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu
 115 120 125
 Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly
 130 135 140
 Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn
 145 150 155 160
 Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His
 165 170 175
 Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg
 180 185 190
 Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser
 195 200 205
 Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
 210 215 220

<210> 102

<211> 220

<212> PRT

<213> Homo sapiens

<400> 102

Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu Ala Gly
 1 5 10 15
 His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn Ser Asn Gly
 20 25 30
 Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly Gly Trp Thr
 35 40 45

Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe Arg Asn Trp
 50 55 60
 Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu
 65 70 75 80
 Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn Tyr Lys Leu
 85 90 95
 Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr Ala Glu Tyr
 100 105 110
 Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg Leu Arg Leu
 115 120 125
 Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp His Asn Gly
 130 135 140
 Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn
 145 150 155 160
 Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His
 165 170 175
 Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys
 180 185 190
 His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser
 195 200 205
 Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
 210 215 220
 <210> 103
 <211> 371
 <212> PRT
 <213> Artificial sequence
 <220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic
 <400> 103
 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

[illegible]

<210> 104
 <211> 367
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 104

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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1          5          10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
          20          25          30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
          35          40          45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
          50          55          60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65          70          75          80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
          85          90          95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
          100          105          110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
          115          120          125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
          130          135          140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys
145          150          155          160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
          165          170          175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly
          180          185          190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe
          195          200          205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu
          210          215          220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn
225          230          235          240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr
          245          250          255

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Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg
260 265 270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp
275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr
290 295 300

Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala
305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr
325 330 335

Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly
340 345 350

Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
355 360 365

<210> 105

<211> 53

<212> PRT

<213> Homo sapiens

<400> 105

Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu
1 5 10 15

Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile
20 25 30

Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr
35 40 45

Asp Val Glu Ala Gln
50

<210> 106

<211> 105

<212> PRT

<213> Homo sapiens

<400> 106

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg
1 5 10 15

Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly
20 25 30

Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro
35 40 45

Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu
50 55 60

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys
100 105

<210> 107

<211> 192

<212> PRT

<213> Homo sapiens

<400> 107

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro
180 185 190

<210> 108

<211> 196

<212> PRT

<213> Homo sapiens

<400> 108

Pro Tyr Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp
 1 5 10 15
 Asp Ser Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn
 20 25 30
 Thr Gln Trp Leu Met Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys
 35 40 45
 Lys Glu Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala
 50 55 60
 Val Met Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln
 65 70 75 80
 Thr Arg Lys Leu Thr Asp Val Glu Ala Gln Val Leu Asn Gln Thr Thr
 85 90 95
 Arg Leu Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu
 100 105 110
 Glu Lys Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp
 115 120 125
 Lys Asn Ser Phe Leu Glu Lys Lys Val Leu Ala Met Glu Asp Lys His
 130 135 140
 Ile Ile Gln Leu Gln Ser Ile Lys Glu Glu Lys Asp Gln Leu Gln Val
 145 150 155 160
 Leu Val Ser Lys Gln Asn Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile
 165 170 175
 Val Thr Ala Thr Val Asn Asn Ser Val Leu Gln Lys Gln Gln His Asp
 180 185 190
 Leu Met Glu Thr
 195

<210> 109
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 109

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg
 1 5 10 15
 Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly
 20 25 30
 Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro
 35 40 45
 Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu
 50 55 60

LVM 205654

65

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys
100 105

<210> 110

<211> 192

<212> PRT

<213> Homo sapiens

<400> 110

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro
180 185 190

<210> 111

<211> 135

<212> PRT

<213> Homo sapiens

<400> 111

Asp Ala Ser Thr Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn
 1 5 10 15
 Leu Lys Asp Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln
 20 25 30
 Leu Val Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu
 35 40 45
 Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met
 50 55 60
 Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu
 65 70 75 80
 Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met Leu Lys
 85 90 95
 Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr
 100 105 110
 Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu Leu Glu Glu Gln
 115 120 125
 Cys Leu Arg Ile Phe Ser Arg
 130 135

<210> 112
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 112

Glu Leu Glu Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile
 1 5 10 15
 Glu Thr Leu Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu
 20 25 30
 Val Lys Leu Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr
 35 40 45
 Gln Leu Tyr Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn
 50 55 60
 Ala Leu Glu Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln Thr Ala
 65 70 75 80
 Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu His Lys Tyr
 85 90 95
 Gln His Leu Ala Thr
 100

<210> 113
 <211> 493
 <212> PRT
 <213> Homo sapiens

<400> 113

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala	Ala		
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Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr	Glu	Glu		
			20					25					30				
Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys	Arg	Ala	Gly		
		35					40					45					
Glu	Ser	Gln	Asp	Lys	Gys	Thr	Tyr	Thr	Phe	Ile	Val	Pro	Gln	Gln	Arg		
	50					55					60						
Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu	Pro	Glu	Val	Leu	Leu		
65					70					75					80		
Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu	Leu	Leu	Asn	Asn	Glu	Leu		
				85					90					95			
Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr	Leu	Gln	Gln	Leu	Val	Glu	Val		
			100					105						110			
Asp	Gly	Gly	Ile	Val	Ser	Glu	Val	Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg		
		115					120					125					
Asn	Met	Asn	Ser	Arg	Val	Thr	Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu		
	130					135					140						
Ile	Ile	Arg	Lys	Arg	Asp	Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn		
145					150					155					160		
Arg	Ile	Leu	Asn	Gln	Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr		
			165						170					175			
Lys	Asp	Leu	Glu	His	Lys	Tyr	Gln	His	Leu	Ala	Thr	Leu	Ala	His	Asn		
		180						185					190				
Gln	Ser	Glu	Ile	Ile	Ala	Gln	Leu	Glu	Glu	His	Cys	Gln	Arg	Val	Pro		
		195					200					205					
Ser	Ala	Arg	Pro	Val	Pro	Gln	Pro	Pro	Pro	Ala	Ala	Pro	Pro	Arg	Val		
	210					215					220						
Tyr	Gln	Pro	Pro	Thr	Tyr	Asn	Arg	Ile	Ile	Asn	Gln	Ile	Ser	Thr	Asn		
225					230					235					240		
Glu	Ile	Gln	Ser	Asp	Gln	Asn	Leu	Lys	Val	Leu	Pro	Pro	Pro	Leu	Pro		
			245						250					255			
Thr	Met	Pro	Thr	Leu	Thr	Ser	Leu	Pro	Ser	Ser	Thr	Asp	Lys	Pro	Ser		
			260					265					270				
Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly	His	Asp	Thr		
		275					280					285					
Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn	Arg	Leu	Met	Gln		
	290					295					300						

Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln
 305 310 315 320
 Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr
 325 330 335
 Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu
 340 345 350
 Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr
 355 360 365
 Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe
 370 375 380
 Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr
 385 390 395 400
 His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe
 405 410 415
 Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His
 420 425 430
 Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
 435 440 445
 Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp
 450 455 460
 Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
 465 470 475 480
 Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
 485 490

<210> 114
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 114

Thr Asn Lys Leu Glu Arg Gln Met Leu Met Gln Ser Arg Glu Leu Gln
 1 5 10 15
 Arg Leu Gln Gly Arg Asn Arg Ala Leu Glu Thr Arg Leu Gln Ala Leu
 20 25 30
 Glu Ala Gln His Gln Ala Gln Leu Asn Ser Leu Gln Glu Lys Arg Glu
 35 40 45
 Gln Leu His Ser Leu Leu
 50

<210> 115
 <211> 145
 <212> PRT

<213> Homo sapiens

<400> 115

Thr Gln Gln Val Lys Gln Leu Glu Gln Ala Leu Gln Asn Asn Thr Gln
1 5 10 15

Trp Leu Lys Lys Leu Glu Arg Ala Ile Lys Thr Ile Leu Arg Ser Lys
20 25 30

Leu Glu Gln Val Gln Gln Gln Met Ala Gln Asn Gln Thr Ala Pro Met
35 40 45

Leu Glu Leu Gly Thr Ser Leu Leu Asn Gln Thr Thr Ala Gln Ile Arg
50 55 60

Lys Leu Thr Asp Met Glu Ala Gln Leu Leu Asn Gln Thr Ser Arg Met
65 70 75 80

Asp Ala Gln Met Pro Glu Thr Phe Leu Ser Thr Asn Lys Leu Glu Asn
85 90 95

Gln Leu Leu Leu Gln Arg Gln Lys Leu Gln Gln Leu Gln Gly Gln Asn
100 105 110

Ser Ala Leu Glu Lys Arg Leu Gln Ala Leu Glu Thr Lys Gln Gln Glu
115 120 125

Glu Leu Ala Ser Ile Leu Ser Lys Lys Ala Lys Leu Leu Asn Thr Leu
130 135 140

Ser
145

<210> 116

<211> 465

<212> DNA

<213> Homo sapiens

<400> 116

gccccatggag agactgcctg caggccctgg aggatggcca cgacaccagc tccatctacc 60

tggtgaagcc ggagaacacc aaccgcctca tgcaggtgtg gtgcgaccag agacacgacc 120

ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180

gggagacgta caagcaagg tttgggaaca ttgacggcga atactggctg ggctggaga 240

acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactggt 300

ccggccgcaa agtctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360

ataagctgcg gctggggcgc taccatggca atgcgggtga ctctttaca tggcacaacg 420

gcaagcagtt caccacccag gacagagatc atgatgtcta cacag 465

<210> 117

<211> 305

<212> DNA

<213> Homo sapiens

<400> 117

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ggattgccag gagctgttcc aggttgggga gaggcagagt ggactatttg aaatccagcc      60
tcaggggtct ccgccatttt tggatgaactg caagatgacc tcagatggag gctggacagt      120
aattcagagg cgccacgatg gctcagtgga cttcaaccgg ccctkggtag cctacaaggc      180
ggtgggtttt ggggatcccc acggcgagtt ctggcttggg tcttggagaa aggkgcatag      240
catcacgggg ggaccggaac agccgmctgg ccgtgcaamc tgcgggggact gggatgggca      300
aacgc                                             305

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<210> 118

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (224)..(244)

<223> "n" may be any nucleotide

<220>

<221> misc_feature

<222> (347)..(347)

<223> "n" may be any nucleotide

<220>

<221> misc_feature

<222> (353)..(353)

<223> "n" may be any nucleotide

<220>

<221> misc_feature

<222> (384)..(384)

<223> "n" may be any nucleotide

<220>

<221> misc_feature

<222> (400)..(400)

<223> "n" may be any nucleotide

<220>

<221> misc_feature

<222> (446)..(446)

<223> "n" may be any nucleotide

<400> 118

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attataagct gcggtggtgg cgataccatg gcaatgcggg tgactccttt acatggcaca      60
acggcaagca gttcaccacc ctggacagag atcatgatgt ctacacagga aactgtgccc      120
actaccagaa gggaggctgg tggatataacg cctgtgcccc ctccaacctc aaccgggggc      180
tggataccgc gggggcatta ccggagccgc taccaggacg gagngtactg ggctgagttc      240

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cgaggaggct cttactcact caaggaaaacg tggatgatgat gatccgaccg aaccccaaca 300
 ccttccacta agccagctcc ccctcctgac ctctccgtgg ccattgncag gangcccacc 360
 ctggtcacgc tggccacagc acanagaaca actcctcacn agttcatcct gaggctggga 420
 ggaccgggat gctggattct gttttnccga agtcactg 458

<210> 119
 <211> 173
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 119
 tataagctgc ggctggggcg ataccatggc aatgcgggtg actcctttac atggcacaac 60
 ggcaagcagt tcaccaccct ggacagagat catgatgtct acacaggaaa ctgtgcccac 120
 taccagaagg gaggctgggtg gtataacgcc tgtgcccact ccaacctcaa ccg 173

<210> 120
 <211> 638
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 120
 gcccatggag agactgcctg caggccctgg aggatggcca cgacaccagc tccatctacc 60
 tggatgaagcc ggagaacacc aaccgcctca tgcaggtgtg gtgcgaccag agacacgacc 120
 ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgtaacttc ttcaggaact 180
 gggagacgta caagcaaggg tttgggaaca ttgacggcga atactggctg ggccctggaga 240
 acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactggt 300
 ccggccgcaa agtctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360
 ataagctgcg gctggggcgc taccatggca atgcgggtga ctctttaca tggcacaacg 420
 gcaagcagtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggctg 480
 gggcgatacc atggcaatgc gggtgactcc ttacatggc acaacggcaa gcagttcacc 540
 accctggaca gagatcatga tgtctacaca ggaaactgtg cccactacca gaagggaggc 600
 tggatggata acgcctgtgc ccaactcaac ctcaaccg 638

<210> 121

<211> 4045
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ().().
 <223> Synthetic

<400> 121
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 ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180
 gggagacgta caagcaaggg tttgggaaca ttgacggcga atactggctg ggcctggaga 240
 acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactggt 300
 ccggccgcaa agtcctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360
 ataagctgcg gctggggcgc taccatggca atgcgggtga ctccctttaca tggcacaacg 420
 gcaagcagtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggctg 480
 gggcgatacc atggcaatgc gggtgactcc tttacatggc acaacggcaa gcagttcacc 540
 accctggaca gagatcatga tgtctacaca ggaaactgtg cccactacca gaaggggaggc 600
 tgggtggtata acgcctgtgc ccactccaac ctcaaccgga aaaagagagg aagagaaacc 660
 atttagagac tgtgcagatg tatatcaagc tggttttaat aaaagtggaa tctacactat 720
 ttatattaat aatatgccag aacccaaaaa ggtgttttgc aatatggatg tcaatggggg 780
 aggttggact gtaatacaac atcgtgaaga tggaaagtcta gatttccaaa gaggctggaa 840
 ggaatataaa atgggttttg gaaatccctc cgggtgaatat tggctgggga atgagtttat 900
 ttttgccatt accagtcaga ggcagtacat gctaagaatt gagttaatgg actgggaagg 960
 gaaccgagcc tattcacagt atgacagatt ccacatagga aatgaaaagc aaaactatag 1020
 gttgtattta aaaggtcaca ctgggacagc aggaaaacag agcagcctga tcttacacgg 1080
 tgctgatttc agcactaaag atgctgataa tgacaactgt atgtgcaaat gtgccctcat 1140
 gttaacagga ggatggtggt ttgatgcttg tggccctcc aatctaaatg gaatgttcta 1200
 tactgcggga caaaaccatg gaaaactgaa tgggataaag tggcactact tcaaagggcc 1260
 cagttactcc ttacgttcca caactatgat gattcgacct ttagattttt gaaagcgcaa 1320
 tgtcagaagc gattatgaaa gcaacaaaga aatccggaga agctgccagg tgagaaaactg 1380
 tttgaaaact tcagaagcaa acaatattgt ctcccttcca gcaataagtg gtagttatgt 1440
 gaagtcacca aggttcttga ccgtgaatct ggagccggtt gagttcacaa gagtctctac 1500

ttgggggtgac agtgctcacg tggctcgact atagaaaact ccactgactg tcgggcttta	1560
aaaaggggaag aaactgctga gcttgctgtg cttcaaacta ctactggacc ttatttttga	1620
actatggtag ccagatgata aatatggtta atttcatgta aaacagaaaa aaagagtga	1680
aaagagaata tacatgaaga atagaaacaa gcctgccata atccttttga aaagatgtat	1740
tataccagtg aaaaggcggtt atatctatgc aaacctacta acaaattata ctgttgacaca	1800
attttgataa aaatttagaa cagcattgtc ctctgagttg gttaaagtgtt aatggatttc	1860
agaagcctaa ttccagtatc atacttacta gttgatttct gcttaccat cttcaaatga	1920
aaattccatt tttgtaagcc ataatagaact gtagtacatg gacaataagt gtgtggtaga	1980
aacaaactcc attactctga tttttgatac agttttcaga aaaagaaatg aacataatca	2040
agtaaggatg tatgtggtga aaacttacca ccccatact atggttttca tttactctaa	2100
aaactgattg aatgatatat aaatatattt atagcctgag taaagttaaa agaagttaaa	2160
atatatcatc aagttcttaa aataatatac atgcatttaa tatttccttt gatattatac	2220
aggaaagcaa tattttggag tatgttaagt tgaagtaaaa ccaagtactc tggagcagtt	2280
cattttacag tatctacttg catgtgtata catatgta acttcattat tttaaaaata	2340
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tgaacatgc ttaccagatt cacactgttc cagtgtctat aaaagaaaca ctttgaagtc	2460
tataaaaaat aaaataatta taaatatcat tgtacatagc atgtttatat ctgcaaaaaa	2520
cctaatagct aattaatctg gaatatgcaa cattgtcctt aattgatgca aataacacaa	2580
atgctcaaag aaatctacta tatcccttaa tgaatacat cattcttcat atatttctcc	2640
ttcagtcctt tcccttaggc aatttttaatt ttttaaaaat tattatcagg ggagaaaaat	2700
tggcaaaact attatatgta agggatatat atatacaaaa agaaaattaa tcatagtcac	2760
ctgactaaga aattctgact gctagttgcc ataaataact caatggaaat attcctatgg	2820
gataatgtat tttaaagtga tttttggggt gcttgaagtt actgcattat tttatcaaga	2880
agttctctct gcctgtaagt gtccaagggt atgacagtaa acagttttta ttaaaacatg	2940
agtcactatg ggatgagaaa attgaaataa agctactggg cctcctctca taaaagagac	3000
agttgttggc aaggtagcaa taccagtttc aaacttgggtg acttgatcca ctatgcctta	3060
atggtttctt ccatttgaga aaataaagct attcacattg ttaagaaaaa tactttttta	3120
agtttaccat caagtctttt ttatatattt gtgtctgtat tctaccctt tttgccttac	3180
aagtgatatt tgcaggattt ataccatttt tctattcttg gtggcttctt catagcaggt	3240

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aagcctctcc ttctaaaaac ttctcaactg ttttcattta agggaaagaa aatgagtatt 3300
ttgtcctttt gtgttcctac agacactttc ttaaaccagt ttttggataa agaatactat 3360
ttccaaactc atattacaaa aacaaaataa aataataaaa aaagaaagca tgatatttac 3420
tgttttgttg tctgggtttg agaaatgaaa tattgtttcc aattatttat aataaatcag 3480
tataaaatgt tttatgattg ttatgtgtat tatgtaatac gtacatgttt atggcaattt 3540
aacatgtgta ttcttttcat ttaattgttt cagaatagga taattaggta ttcgaatttt 3600
gtcttttaaaa ttcatgtggt ttctatgcaa agttcttcat atcatcacia cattatttga 3660
tttaaataaa attgaaagtg cacccatggc agaaggagga gggcagaatc atcacgaagt 3720
ggatgaagttc atggatgtct atcagcgcag ctactgcat ccaatcgaga ccctgggtgga 3780
catcttccag gagtaccctg atgagatcga gtacatcttc aagccatcct gtgtgcccct 3840
gatgcgatgc gggggctgct gcaatgacga gggcctggag tgtgtgcca ctgaggagtc 3900
caacatcacc atgcagatta tgcggatcaa acctaccaa ggccagcaca taggagagat 3960
gagcttccca cagcacaaca aatgtgaatg cagaccaaag aaagatagag caagacaaga 4020
aaaatgtgac aagccgaggc ggtga 4045

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<210> 122
<211> 280
<212> PRT
<213> Artificial sequence

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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

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<400> 122

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Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1           5           10          15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20          25          30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35          40          45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50          55          60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65          70          75          80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
85          90          95
Val Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile

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100	105	110
Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly		
115	120	125
Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp		
130	135	140
Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu		
145	150	155
Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp		
165	170	175
Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu		
180	185	190
Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser		
195	200	205
Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn		
210	215	220
Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn		
225	230	235
Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn		
245	250	255
Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr		
260	265	270
Val Ala Lys Glu Glu Gln Ile Ser		
275	280	

<210> 123
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 123

Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly		
1	5	10
Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu		
20	25	30
Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr		
35	40	45
Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp		
50	55	60
Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu		
65	70	75
Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu		
85	90	95

Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr
 100 105 110

Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu
 115 120 125

Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His
 130 135 140

Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys
 145 150 155 160

Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly
 165 170 175

Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly
 180 185 190

Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser
 195 200 205

Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe
 210 215 220

<210> 124
 <211> 1506
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 124
 atgtggcaga ttgttttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60
 aactttcgga agagcatgga cagcatagga aagaagcaat atcagggtcca gcatgggtcc 120
 tgcagctaca ctttctctct gccagagatg gacaactgcc gctcttcttc cagcccctac 180
 gtgtccaatg ctgtgcagag ggacgcgccg ctccaatacg atgactcggt gcagaggctg 240
 caagtgctgg agaacatcat ggaaaacaac actcagtggc taatgaagggt agagaatata 300
 tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag 360
 acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420
 aagttaactg atgtggaagc ccaagtatta aatcagacca cgagacttga acttcagctc 480
 ttggaacact ccctctcgac aaacaaattg gaaaaacaga ttttggacca gaccagtga 540
 ataaacaaat tgcaagataa gaacagtttc ctagaaaaga aggtgctagc tatggaagac 600
 aagcacatca tccaactaca gtcaataaaa gaagagaaag atcagctaca ggtgttagta 660
 tccaagcaga attccatcat tgaagaactc gaaaaaaaaa tagtgactgc cacggtgaat 720

```

aattcagttc ttcagaagca gcaacatgat ctcatggaga cagttaataa cttactgact      780
atgatgtcca catcaaacgc agctaaggac cccactgttg ctaaagaaga acaaatcagc      840
gaggaagaga aaccatttag agactgtgca gatgtatatc aagctgggtt taataaaaagt      900
ggaatctaca ctatttatat taataatatg ccagaaccca aaaaggtggt ttgcaatatg      960
gatgtcaatg ggggagggtg gactgtaata caacatcgtg aagatggaag tctagatttc     1020
caaagaggct ggaaggaata taaaatgggt tttggaaatc cctccggtga atattggctg     1080
gggaatgagt ttatTTTTgc cattaccagt cagaggcagt acatgctaag aattgagtta     1140
atggactggg aagggaaaccg agcctattca cagtatgaca gattccacat aggaaatgaa     1200
aagcaaaaact ataggttgta tttaaaaggt cacactggga cagcaggaaa acagagcagc     1260
ctgatcttac acggtgctga tttcagcact aaagatgctg ataatgacaa ctgtatgtgc     1320
aaatgtgccc tcatgttaac aggaggatgg tggtttgatg cttgtggccc ctccaatcta     1380
aatggaatgt tctatactgc gggacaaaac catggaaaac tgaatgggat aaagtggcac     1440
tacttcaaag ggcccagtta ctccctacgt tccacaacta tgatgattcg acctttagat     1500
ttttga                                                                    1506

```

```

<210> 125
<211> 501
<212> PRT
<213> Artificial sequence

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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

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```

<400> 125

```

```

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1          5          10          15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20          25          30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35          40          45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50          55          60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65          70          75          80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
85          90          95

```

Val	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met	Val	Glu	Ile	100	105	110
Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile	Glu	Ile	Gly	115	120	125
Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys	Leu	Thr	Asp	130	135	140
Val	Glu	Ala	Gln	Val	Leu	Asn	Gln	Thr	Thr	Arg	Leu	Glu	Leu	Gln	Leu	145	150	155
Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln	Ile	Leu	Asp	165	170	175
Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser	Phe	Leu	Glu	180	185	190
Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln	Leu	Gln	Ser	195	200	205
Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser	Lys	Gln	Asn	210	215	220
Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala	Thr	Val	Asn	225	230	235
Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	His	Asp	Leu	Met	Glu	Thr	Val	Asn	245	250	255
Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Ala	Ala	Lys	Asp	Pro	Thr	260	265	270
Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Glu	Glu	Glu	Lys	Pro	Phe	Arg	Asp	275	280	285
Cys	Ala	Asp	Val	Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly	Ile	Tyr	Thr	290	295	300
Ile	Tyr	Ile	Asn	Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe	Cys	Asn	Met	305	310	315
Asp	Val	Asn	Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	His	Arg	Glu	Asp	Gly	325	330	335
Ser	Leu	Asp	Phe	Gln	Arg	Gly	Trp	Lys	Glu	Tyr	Lys	Met	Gly	Phe	Gly	340	345	350
Asn	Pro	Ser	Gly	Glu	Tyr	Trp	Leu	Gly	Asn	Glu	Phe	Ile	Phe	Ala	Ile	355	360	365
Thr	Ser	Gln	Arg	Gln	Tyr	Met	Leu	Arg	Ile	Glu	Leu	Met	Asp	Trp	Glu	370	375	380
Gly	Asn	Arg	Ala	Tyr	Ser	Gln	Tyr	Asp	Arg	Phe	His	Ile	Gly	Asn	Glu	385	390	395
Lys	Gln	Asn	Tyr	Arg	Leu	Tyr	Leu	Lys	Gly	His	Thr	Gly	Thr	Ala	Gly	405	410	415

Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp
 420 425 430
 Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly
 435 440 445
 Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe
 450 455 460
 Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His
 465 470 475 480
 Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile
 485 490 495
 Arg Pro Leu Asp Phe
 500

<210> 126
 <211> 648
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

<400> 126

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140
 Pro Arg Arg Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu

145		150		155		160									
Val	Leu	Ala	Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile
			165						170					175	
Gly	Lys	Lys	Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe
			180					185					190		
Leu	Leu	Pro	Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Ser	Pro	Tyr	Val
		195					200					205			
Ser	Asn	Ala	Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val
	210					215					220				
Gln	Arg	Leu	Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp
225				230						235					240
Leu	Met	Lys	Val	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met
			245						250					255	
Val	Glu	Ile	Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile
			260					265					270		
Glu	Ile	Gly	Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys
		275					280					285			
Leu	Thr	Asp	Val	Glu	Ala	Gln	Val	Leu	Asn	Gln	Thr	Thr	Arg	Leu	Glu
	290					295					300				
Leu	Gln	Leu	Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln
305					310					315					320
Ile	Leu	Asp	Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser
			325						330					335	
Phe	Leu	Glu	Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln
			340					345					350		
Leu	Gln	Ser	Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser
		355					360					365			
Lys	Gln	Asn	Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala
	370					375					380				
Thr	Val	Asn	Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	His	Asp	Leu	Met	Glu
385					390					395					400
Thr	Val	Asn	Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Ala	Ala	Lys
				405					410					415	
Asp	Pro	Thr	Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Glu	Glu	Glu	Lys	Pro
			420					425					430		
Phe	Arg	Asp	Cys	Ala	Asp	Val	Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly
		435					440					445			
Ile	Tyr	Thr	Ile	Tyr	Ile	Asn	Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe
	450					455					460				

Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg
 465 470 475 480
 Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met
 485 490 495
 Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile
 500 505 510
 Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met
 515 520 525
 Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile
 530 535 540
 Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly
 545 550 555 560
 Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser
 565 570 575
 Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met
 580 585 590
 Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn
 595 600 605
 Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile
 610 615 620
 Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr
 625 630 635 640
 Met Met Ile Arg Pro Leu Asp Phe
 645